

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Stocco, Douglas M.
Clark, Barbara J.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION OF
STEROIDOGENESIS

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:
(B) COMPUTER:
(C) OPERATING SYSTEM:
(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 33,732
(C) REFERENCE/DOCKET NUMBER: 043375.0006/DLM

(ix) TELECOMMUNICATION INFORMATION:

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5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGACCCAC GCGTCCGCTC AGGACCTTGA AAGGCTCAGG AAGAACAACC CTTGAGCACC 60

TCAGCACTCA GCATGTTCTT CGCTACGTTT AAGCTGTGTG CTGGAAGCTC CTATAGACAT 120

20 ATGCGGAATA TGAAAGGATT AAGGCACCAA GCTGTGCTGG CCATTGGCCA AGAGCTCAAC 180

TGGAGAGCAC TGGGGGATTC CAGTCCCGGG TGGATGGGTC AAGTTCGACG TCGGAGCTCT 240

25 CTGCTTGTTT CTCAACTGGA AGCAACACTC TATAGTGACC AGGAGCTGTC CTACATCCAG 300

CAGGGAGAGG TGGCTATGCA GAAGGCCTTG GGCATACTCA ACAACCAGGA AGGCTGGAAG 360

AAGGAAAGCC AGCAGGAGAA CGGGGACGAA GTGCTAAGTA AGATGGTGCC AGATGTGGGC 420

30 AAGGTGTTTC GCTTGGAGGT GGTGGTAGAC CAGCCCATGG ACAGACTCTA TGAAGAACTT 480

GTGGACCGCA TGGAGGCCAT GGGAGAGTGG AACCCAAATG TCAAGGAGAT CAAGGTCCTG 540

35 CAGAGGATTG GAAAAGACAC GGTCATCACT CATGAGCTGG CTGCGGCGGC AGCAGGCAAC 600

	CTGGTGGGGC CTCGAGACTT CGTGAGCGTG CGCTGTACCA AGCGCAGAGG TTCCACCTGT	660
	GTGCTGGCAG GCATGGCCAC ACATTTTGGG GAGATGCCGG AGCAGAGTGG TGTCAACAGA	720
5	GCTGAACACG GCCCCACCTG CATGGTGCTT CATCCACTGG CTGGAAGTCC CTCCAAGACT	780
	AAACTCACTT GGCTGCTCAG TATTGACCTG AAGGGGTGGC TGCCGAAGAC AATCATCAAC	840
	CAGGTCCTAT CGCAGACCCA GATAGAGTTC GCCAACCACC TGC GCAAGCG CCTGGAAGCC	900
10	AGCCCTGCCT CTGAGGCCCA GTGTTAAGGA CTGTCCACCA CATTGACCTG CAAATCATTG	960
	GAAGCTCTCA CAGGAAGCCT GCAAGTCTGT CCATCTTCAG CTAACAGCAT CGGGAGGGGT	1020
15	GGTAGTCAGG AGACACTAGG ACTGACTGGT AAAATCAGGA TCAGCAAAAT AGAAATGAGG	1080
	CTTAGAATAA AAGTTCTCTA GTGTCTCCCA CTGCATAGCT GTGAAGGCTA AGGGATAAGT	1140
	AGCTATGAAA CCTTTTCATCT AGGCTTGTAT ATGCTGACCT AAAAGACACC AGCAGCTACG	1200
20	AACAGGGGAT GCTAAGGATC GGGAACTGTT GTCTTACCAG CTCCAAATGT CACTACCTGA	1260
	AGGCAGTGTG CACACAAAGC AAGGTCTTGC CTAGGAAACT CTGTAAAAGT TCTCCTCTGT	1320
25	AAAAGGCCAG AACTTGAATG AACTACCTA CAAAGGGCCT TTCCAGAGTA TTCCAACCTT	1380
	TCTCTGAGGA GAAATGAAAC CATCATTGTG CCGACTTCCC TACTAATCCC ATGACAATAA	1440
30	AGAACATACA TAAAAAAAAA AAAAAA	1466

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10 Met Phe Leu Ala Thr Phe Lys Leu Cys Ala Gly Ser Ser Tyr Arg His
1 5 10 15

Met Arg Asn Met Lys Gly Leu Arg His Gln Ala Val Leu Ala Ile Gly
20 25 30

15 Gln Glu Leu Asn Trp Arg Ala Leu Gly Asp Ser Ser Pro Gly Trp Met
35 40 45

Gly Gln Val Arg Arg Arg Ser Ser Leu Leu Gly Ser Gln Leu Glu Ala
50 55 60

20 Thr Leu Tyr Ser Asp Gln Glu Leu Ser Tyr Ile Gln Gln Gly Glu Val
65 70 75 80

Ala Met Gln Lys Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys
25 85 90 95

Lys Glu Ser Gln Gln Glu Asn Gly Asp Glu Val Leu Ser Lys Met Val
100 105 110

30 Pro Asp Val Gly Lys Val Phe Arg Leu Glu Val Val Val Asp Gln Pro
115 120 125

Met Asp Arg Leu Tyr Glu Glu Leu Val Asp Arg Met Glu Ala Met Gly
130 135 140

35

Glu Trp Asn Pro Asn Val Lys Glu Ile Lys Val Leu Gln Arg Ile Gly
 145 150 155 160

Lys Asp Thr Val Ile Thr His Glu Leu Ala Ala Ala Ala Gly Asn
 165 170 175

Leu Val Gly Pro Arg Asp Phe Val Ser Val Arg Cys Thr Lys Arg Arg
 180 185 190

Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
 195 200 205

Pro Glu Gln Ser Gly Val Ile Arg Ala Glu His Gly Pro Thr Cys Met
 210 215 220

Val Leu His Pro Leu Ala Gly Ser Pro Ser Lys Thr Lys Leu Thr Trp
 225 230 235 240

Leu Leu Ser Ile Asp Leu Lys Gly Trp Leu Pro Lys Thr Ile Ile Asn
 245 250 255

Gln Val Leu Ser Gln Thr Gln Ile Glu Phe Ala Asn His Leu Arg Lys
 260 265 270

Arg Leu Glu Ala Ser Pro Ala Ser Glu Ala Gln Cys
 275 280

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5 Ala Glu His Gly Pro Thr Cys Met Val Leu His Pro Leu Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

20 Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35

Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
1 5 10 15

Pro Glu Gln

5

(2) INFORMATION FOR SEQ ID NO:6:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20

Asn Gln Glu Gly Trp Lys

1 5

(2) INFORMATION FOR SEQ ID NO:7:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35

Ala Glu His Gly Pro Thr Cys Met Val

1 5

5 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ile Leu Asn Asn Gln Glu Gly Trp Lys Lys Glu

1 5 10

20 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

30

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: one-of(3, 12, 15, 18)

(D) OTHER INFORMATION: /mod_base= OTHER

35 /note= "N = (A or C or G or T/U) or (unknown or other)"

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 6

(D) OTHER INFORMATION: /mod_base= OTHER

5 /note= "R = A or G"

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: one-of(9, 21)

10 (D) OTHER INFORMATION: /mod_base= OTHER

/note= "Y = C or T/U"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15

GCNGARCAYG GNCCNACNTG YATGG

25

(2) INFORMATION FOR SEQ ID NO:10:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(ix) FEATURE:

30

(A) NAME/KEY: modified_base

(B) LOCATION: one-of(5, 17)

(D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

35

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION: one-of(8, 11, 14, 23)
(D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = (A or C or G or T/U) or (unknown or other)"

5

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION: 20
(D) OTHER INFORMATION: /mod_base= OTHER

10

/note= "Y = C or T/U"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCATRCANGT NGGNCCRTGY TCNGC

25

15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

25

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION: 3
(D) OTHER INFORMATION: /mod_base= OTHER

30

/note= "Y = C or T/U"

(ix) FEATURE:

(A) NAME/KEY: modified_base

35

(B) LOCATION: one-of(6, 9)

(D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

5

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 12

(D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = (A or C or G or T/U) or (unknown or other)"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAYCARCARG GNTGGAA

17

15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCCANCCYT CYTGRTT

17

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10	AACCAGGAAG GCTGGAAGAA GGAAAGCCAG CAGGAGAACG GGGACGAAGT GCTAAGTAAG	60
	ATGGTGCCAG ATGTGGGCAA GGTGTTTCGC TTGGAGGTGG TGGTAGACCA GCCCATGGAC	120
	AGACTCTATG AAGAACTTGT GGACCGCATG GAGGCCATGG GAGAGTGGAA CCCAAATGTC	180
15	AAGGAGATCA AGGTCCTGCA GAGGATTGGA AAAGACACGG TCATCACTCA TGAGCTGGCT	240
	GCGGCGGCAG CAGGCAACCT GGTGGGGCCT CGAGACTTCG TGAGCGTGCG CTGTACCAAG	300
20	CGCAGAGGTT CCACCTGTGT GCTGGCAGGC ATGGCCACAC ATTTTGGGGA GATGCCGGAG	360
	CAGAGTGGTG TCATCAGAGC TGAACACGGC CCCACCTGCA T	401

25 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "RNA"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

	GUCGACCCAC GCGUCCGCUC AGGACCUUGA AAGGCUCAGG AAGAACAACC CUUGAGCACC	60
5	UCAGCACTUCA GCAUGUUCTU CGCUACGUUC AAGCUGUGUG CUGGAAGCUC CUAUAGACAU	120
	AUGCGGAAUA UGAAAGGAUU AAGGCACCAA GCUGUGCUGG CCAUUGGCCA AGAGTCUAAC	180
	UGGAGAGCAC UGGGGGAUUC CAGUCCCGGG UGGAUGGGUC AAGUUCGACG UCGGAGCUCU	240
10	CUGCUUGGUU CUCAACUGGA AGCAACACUC UAUAGUGACC AGGAGCUGUC CUACAUCCAG	300
	CAGGGAGAGG UGGCUAUGCA GAAGGCTUUG GGCAUACUCA ACAACCAGGA AGGCUGGAAG	360
15	AAGGAAAGCC AGCAGGAGAA CGGGGACGAA GUGCUAAGUA AGAUGGUGCC AGAUGUGGGC	420
	AAGGUGUUUC GCUUGGAGGU GGUGGUAGAC CAGCCCAUGG ACAGACTUCU UGAAGAACUU	480
	GUGGACCGCA UGGAGGCCAU GGGAGAGUGG AACCCAAAUG UCAAGGAGAU CAAGGUCCUG	540
20	CAGAGGAUUG GAAAAGACAC GGUCAUCACU CAUGAGCUGG CUGCGGCGGC AGCAGGCAAC	600
	CUGGUGGGGC CUCGAGACUU CGUGAGCGUG CGCUGUACCA AGCGCAGAGG UUCCACCTUGU	660
25	GUGCUGGCAG GCAUGGCCAC ACAUUUUGGG GAGAUGCCGG AGCAGAGUGG UGUCAUCAGA	720
	GCUGAACACG GCCCCACCTG CAUGGUGCTU CAUCCACUGG CUGGAAGUCC CUCCAAGACU	780
	AAATUCACTU GGCUGCUCAG UAUUGACCUG AAGGGGUGGC UGCCGAAGAC AAUCAUCAAC	840
30	CAGGUCCUUA CGCAGACCCA GAUAGAGUUC GCCAACCACC UGCGCAAGCG CCUGGAAGCC	900
	AGCCCTUGCTU CUGAGGCCCA GUGUUAAGGA CUGUCCACCA CAUUGACCUG CAAAUCAUUG	960
35	GAAGCUCUCA CAGGAAGCTU GCAAGUCUGU CCAUCUUCAG CUAACAGCAU CGGGAGGGGU	1020

	GGUAGUCAGG AGACACUAGG ACUGACUGGU AAAAUCAGGA UCAGCAAAAU AGAAAUGAGG	1080
	CUUAGAAUAA AAGUUCUCUA GUGUCUCCCA CUGCAUAGCU GUGAAGGCUA AGGGAUAGU	1140
5	AGCUAUGAAA CCUUUCAUCU AGGCUUGUUAU AUGCUGACCU AAAAGACACC AGCAGCUACG	1200
	AACAGGGGAU GCUAAGGAUC GGGAACUGUU GUCUUACCAG CUCCAAAUGU CACUACCUGA	1260
10	AGGCAGUGUG CACACAAAGC AAGGUCUUGC CUAGGAAACU CUGUAAAAGU UCUCUCUGU	1320
	AAAAGGCCAG AACUUGAAUG AAACUACCUA CAAAGGGCCU UCCAGAGUA UCCAACUUU	1380
	UCUCUGAGGA GAAAUGAAAC CAUCAUUGUG CCGACUCCC UACUAAUCCC AUGACAAUAA	1440
15	AGAACAUACA UAAAAAAAAA AAAAAA	1466

(2) INFORMATION FOR SEQ ID NO:15:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

(D) TOPOLOGY:

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(ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:15:

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267	GTGGATTAAC CAGGTTCCGC GCGGAGCTC TCTACTCGGT TCTCGGCTGG AAGAGACTCT	326
327	CTACAGTGAC CAGGAGCTGG CCTATCTCCA GCAGGGGGAG GAGGCCATGC AGAAGGCCTT	386
387	GGGCATCCTT AGCAACCAAG AGGGCTGGAA GAAGGAGAGT CAGCAGGACA ATGGGGACAA	446
447	AGTGATGAGT AAAGTGGTCC CAGATGTGGG CAAGGTGTTT CCGCTGGAGG TCGTGGTGGA	506
35	507 CCAGCCCATG GAGAGGCTCT ATGAAGAGCT CGTGGAGCGC ATGGAAGCAA TGGGGGAGTG	566

567 GAACCCCAAT GTCAAGGAGA TCAAGGTCCT GCAGAAGATC GGAAAAGATA CATTATTAC 626
 627 TCACGAGCTG GCTGCCGAGG CAGCAGGAAA CCTGGTGGGG CCCCCTGACT TTGTGAGCGT 686
 687 GCGCTGTGCC AAGCGCCGAG GCTCCACCTG TGTGCTGGCT GGCATGGACA CAGACTTCGG 746
 747 GAACATGCCT GAGCAGAAGG GTGTCATCAG GGCGGAGCAC GGTCCCCTT GCATGGTGCT 806
 807 TCACCCGTTG GCTGGAAGTC CCTCTAAGAC CAACTTACG TGGCTACTCA GCATCGACCT 866
 867 CAAGGGGTGG CTGCCCAAGA GCATCATCAA CCAGGTCCTG TCCCAGACCC AGGTGGATTT 926
 927 TGCCAACCAC CTGCGCAAGC GCCTGGAGTC CCACCCTGCC TCTGAAGCCA GGTGTTGAAG 986
 987 AC 988

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

(ii) MOLECULE TYPE:

- (A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:16:

127 ATGCTGCTAG CGACATTCAA GCTGTGCGCT GGGAGCTCCT ACAGACACAT GCGCAACATG 186
 187 AAGGGGCTGA GGCAACAGGC TGTGATGGCC ATCAGCCAGG AGCTGAACCG GAGGGCCCTG 246
 247 GGGGGCCCCA CCCC 260

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:17:

5

1051 ACTGGAAGCC TGCAAGTCT 1069

(2) INFORMATION FOR SEQ ID NO:18:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

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(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

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SEQUENCE DESCRIPTION: SEQ ID NO:18:

1 MLLATFKLCA GSSYRHRNM KGLRQQAVMA ISQELNRRAL GGPTPSTWIN 50
51 QVRRRSSLLG SRLEETLYSD QELAYLQQGE EAMQKALGIL SNQEGWKES 100
101 QQDNGDKVMS KVVDPVGKVF RLEVVDQPM ERLYEELVER MEAMGEWNP 150
25 151 VKEIKVLQKI GKDTFITHL AAEAAGNLVG PRDFVSVRCA KRRGSTCVLA 200
201 GMATDFGNMP EQKGVIRAEH GPTCMVLHPL AGSPSKTKLT WLLSIDLKGW 250
251 LPKSIINQVL SQTQVDFANHL RKRLESHPA SEARC 285

(2) INFORMATION FOR SEQ ID NO:19:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

35

(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:19:

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agaacaccag gtccaggctg cagctgcggg actcagaggc gaacgttgag gggctcagga 60
aggacgaaga accacccttg agagaagagg cagcagcagc gcggcagcag cagcggcagc 120
gacccccacca ctgccacatt tgccaggaaa caATGCTGCT AGCGACATTC AAGCTGTGCG 180
CTGGGAGCTC CTACAGACAC ATGCGCAACA TGAAGGGGCT GAGGCAACAG GCTGTGATGG 240
CCATCAGCCA GGAGCTGAAC CGGAGGGGCC TGGGGGGCCC CACCCTAGC ACGTGGATTA 300
ACCAGGTTTC GCGGCGGAGC TCTCTACTCG GTTCTCGGCT GGAAGAGACT CTCTACAGTG 360
ACCAGGAGCT GGCCTATCTC CAGCAGGGGG AGGAGGCCAT GCAGAAGGCC TTGGGCATCC 420
TTAGCAACCA AGAGGGCTGG AAGAAGGAGA GTCAGCAGGA CAATGGGGAC AAAGTGATGA 480
GTAAAGTGGT CCCAGATGTG GGCAAGGTGT TCCGGCTGGA GGTCTGTGGT GACCAGCCCA 540
TGGAGAGGCT CTATGAAGAG CTCGTGGAGC GCATGGAAGC AATGGGGGAG TGAACCCCA 600
ATGTCAAGGA GATCAAGGTC CTGCAGAAGA TCGGAAAAGA TACATTCATT ACTCACGAGC 660
TGGCTGCCGA GGCAGCAGGA AACCTGGTGG GGCCCCGTGA CTTTGTGAGC GTGCGCTGTG 720
CCAAGCGCCG AGGCTCCACC TGTGTGCTGG CTGGCATGGC CACAGACTTC GGGAACATGC 780
CTGAGCAGAA GGGTGTCTATC AGGGCGGAGC ACGGTCCCAC TTGCATGGTG CTTACCCCGT 840
TGGCTGGAAG TCCCTCTAAG ACCAACTTA CGTGGCTACT CAGCATCGAC CTCAAGGGGT 900
GGCTGCCCAA GAGCATCATC AACCAGGTCC TGTCACAGAC CCAGGTGGAT TTTGCCAACC 960
ACCTGCGCAA GCGCCTGGAG TCCCACCCTG CCTCTGAAGC CAGGTGTTGA agaccagcct 1020
gctgttccca actgtgcccc gctgcactgg tacacacgct catcaggaga atccctactg 1080
gaagcctgca agtctaagat ctccatctgg tgacagtggg atgggtgggg ttcgtgttta 1140
gagtatgaca ctaggattca gattggtgaa agtttttagt accaagaaaa cagggatgag 1200
ctcttgattt aaaaggtaac ttcattcact gattagctat gacatgaggg ttcaggcccc 1260
ctaaaaataa ttgtaaaact ttttttctgg gcccttatgt acccacctaa aaccatcttt 1320
aaaatgctag tggctgatat ggggtgtggg gatgctaacc acagggcctg agaagtcttg 1380
ctttatgggc tcaagaatgc catgcgctgg cagtacatgt gcacaaagca gaatctcaga 1440
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gcaccccaaca gtgggtgcct tccagaaata tagtccaagc tttctctgtg gaaaaagaca 1560
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